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—o— NO ANTIGEN (SBAS2)

····o··· Mtb32 + Mtb 39 (SBAS2)

···o··· Mtb32 — Mtb 39 FUSION (SBAS2)

—△—— BCG

FIG. 1.

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FIG. 2A.

FIG. 2B.

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FIG. 3.

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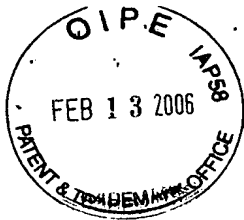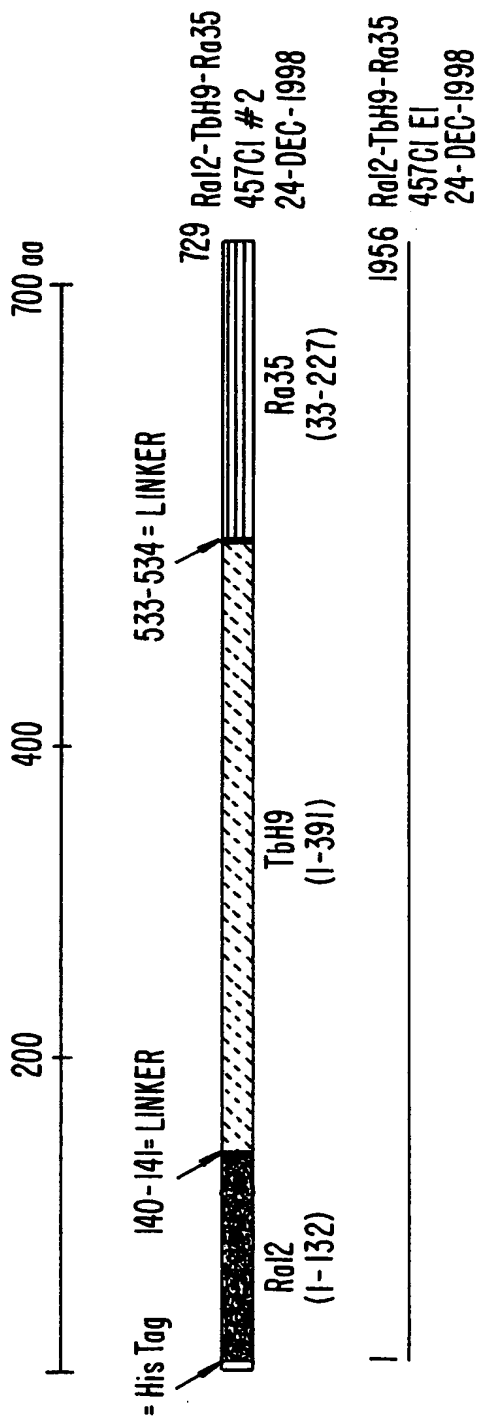Title: FUSION PROTEINS OF MYCOBACTERIUM TUBERCULOSIS
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Ra35 N-terminus DNA

```
gccccgccgg ccttgtcgca ggaccggttc gccgacttcc ccgcgctgcc cctcgacccg tccgcgatgg   70
tcgcccaagt ggggccacag gtggtcaaca tcaacaccaa actgggctac aacaacgccg tgggcgccgg  140
gaccggcatc gtcatcgatc ccaacggtgt cgtgctgacc aacaaccacg tgatcgcggg cgccaccgac  210
atcaatgcgt tcagcgtcgg ctccggccaa acctacgccg tcggtatgac cgcacccagg             280
atgtccagcc gctgcagctg gctgcctacc atcggcgcgg atcggtgggcg gcgtcgcggt            350
tggtgagccc gtcgtcgcga tgggcaacag cgtgtgggcag cccgtgcggt gcctggcagg           420
gtggtcgcgc tcggcccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaaagaca ttgaacgggt  490
tgatccagtt cgatgccgcg atccacccg gtgattcggg cgggcccgtc gtcaacggcc taggacaggt   560
ggtcggtatg aacacggccg cgtcctag                                               588
```

Ra35 N-terminus amino acid sequence

```
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala
                  5                  10                  15                  20

Met Val Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val
          25                  30                  35                  40

Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val Ile Ala
          45                  50                  55                  60                  65

Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Gln Thr Tyr Gly Val Asp Val Val Gly
          70                  75                  80                  85

Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala
          90                  95                  100                 105             110
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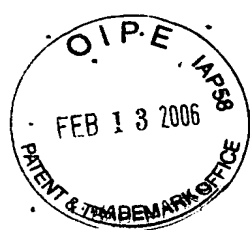
FIG. 4.

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Ile Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly
115   120   125   130

Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
135   140   145   150

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
155   160   165   170   175

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser
180   185   190   195

FIG. 4. (CONTINUED)

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Ra12

```
  1   MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLG   Mtb72f
  1   MHHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLG   Mtb72f-mutSA

 56   LGVVDNNGNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHH   Mtb72f
 56   LGVVDNNGNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHH   Mtb72f-mutSA

                                          TbH9FL
111   PGDVISVTWQTKSFFTRTFNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSAS   Mtb72f
111   PGDVISVTWQTKSFFTRTFNVTLAEGPPAEFMVDFGALPPEINSARMYAGPGSAS   Mtb72f-mutSA

166   LVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSV   Mtb72f
166   LVAAAQMWDSVASDLFSAASAFQSVVWGLTVGSWIGSSAGLMVAAASPYVAWMSV   Mtb72f-mutSA

221   TAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAI   Mtb72f
221   TAGQAELTAAQVRVAAAAYETAYGLTVPPPVIAENRAELMILIATNLLGQNTPAI   Mtb72f-mutSA

276   AVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVE   Mtb72f
276   AVNEAEYGEMWAQDAAAMFGYAAATATATATLLPFEEAPEMTSAGGLLEQAAAVE   Mtb72f-mutSA

331   EASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM   Mtb72f
331   EASDTAAANQLMNNVPQALQQLAQPTQGTTPSSKLGGLWKTVSPHRSPISNMVSM   Mtb72f-mutSA

386   ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSS   Mtb72f
386   ANNHMSMTNSGVSMTNTLSSMLKGFAPAAAAQAVQTAAQNGVRAMSSLGSSLGSS   Mtb72f-mutSA

441   GLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQM   Mtb72f
441   GLGGGVAANLGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQM   Mtb72f-mutSA
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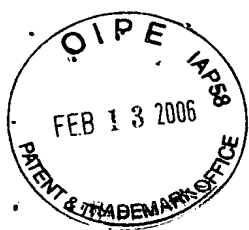
FIG. 5.

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Ra35

```
496  LGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPAL   Mtb72f
496  LGGLPVGQMGARAGGGLSGVLRVPPRPYVMPHSPAAGDIAPPALSQDRFADFPAL   Mtb72f-mutSA

551  PLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNNVIAGATDI   Mtb72f
551  PLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATDI   Mtb72f-mutSA

606  NAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN   Mtb72f
606  NAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGN   Mtb72f-mutSA

661  SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVV   Mtb72f
661  SGGQGGTPRAVPGRVVALGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVV   Mtb72f-mutSA

716  NGLGQVVGMNTAAS   Mtb72f
716  NGLGQVVGMNTAAS   Mtb72f-mutSA
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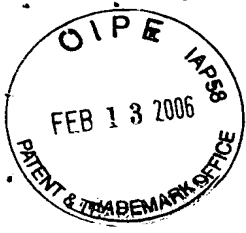
FIG. 5. (CONTINUED)

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```
                  Ra35 N-term
  1   MHHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNA   TbRa35_mat
  1   MHHHHHHAPPALSQDRFADFPALPLDPSAMVAQVGPQVVNINTKLGYNNA   TbRa35_mutSA

 51   VGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQ   TbRa35_mat
 51   VGAGTGIVIDPNGVVLTNNHVIAGATDINAFSVGSGQTYGVDVVGYDRTQ   TbRa35_mutSA

101   DVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVA   TbRa35_mat
101   DVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSGGQGGTPRAVPGRVVA   TbRa35_mutSA

                                                 Ra12 Cterm
151   LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDSGGPVVNGLGQVVGMNTA   TbRa35_mat
151   LGQTVQASDSLTGAEETLNGLIQFDAAIQPGDAGGPVVNGLGQVVGMNTA   TbRa35_mutSA
         end Ra35 Nterm
201   ASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV   TbRa35_mat
201   ASDNFQLSQGGQGFAIPIGQAMAIAGQIRSGGGSPTVHIGPTAFLGLGVV   TbRa35_mutSA

251   DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH   TbRa35_mat
251   DNNGNGARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGH   TbRa35_mutSA

301   HPGDVISVTWQTKSGGTRTGNVTLAEGPPA   end    TbRa35_mat
301   HPGDVISVTWQTKSGGTRTGNVTLAEGPPA   Ra12   TbRa35_mutSA
```
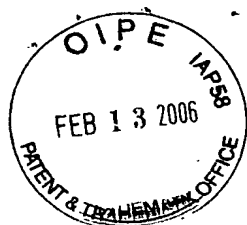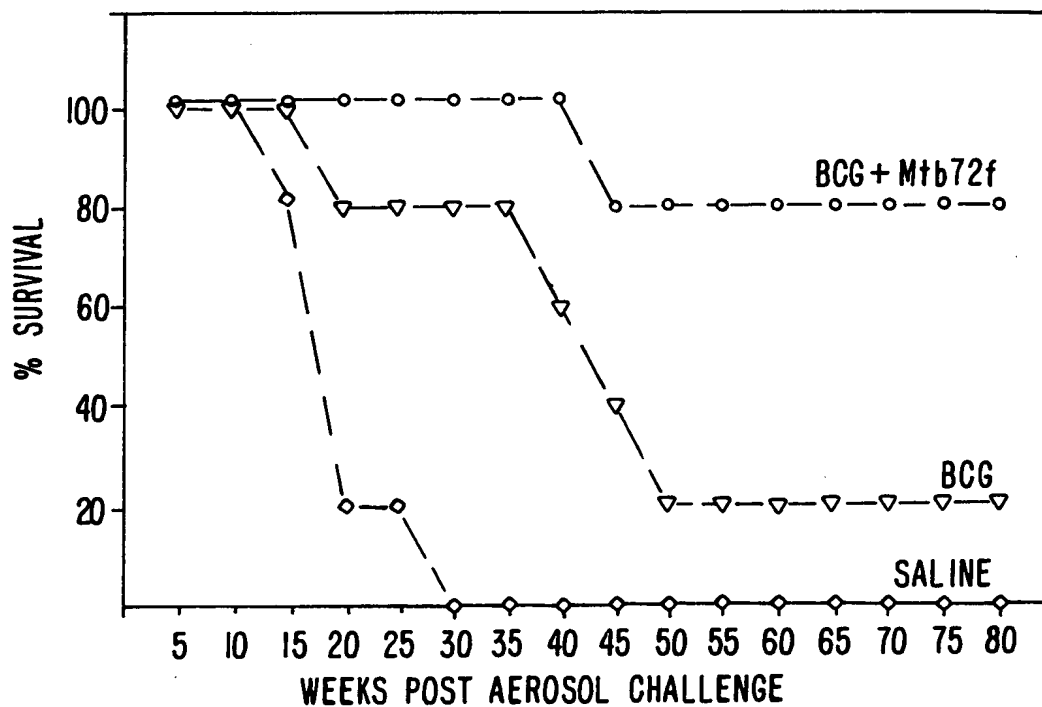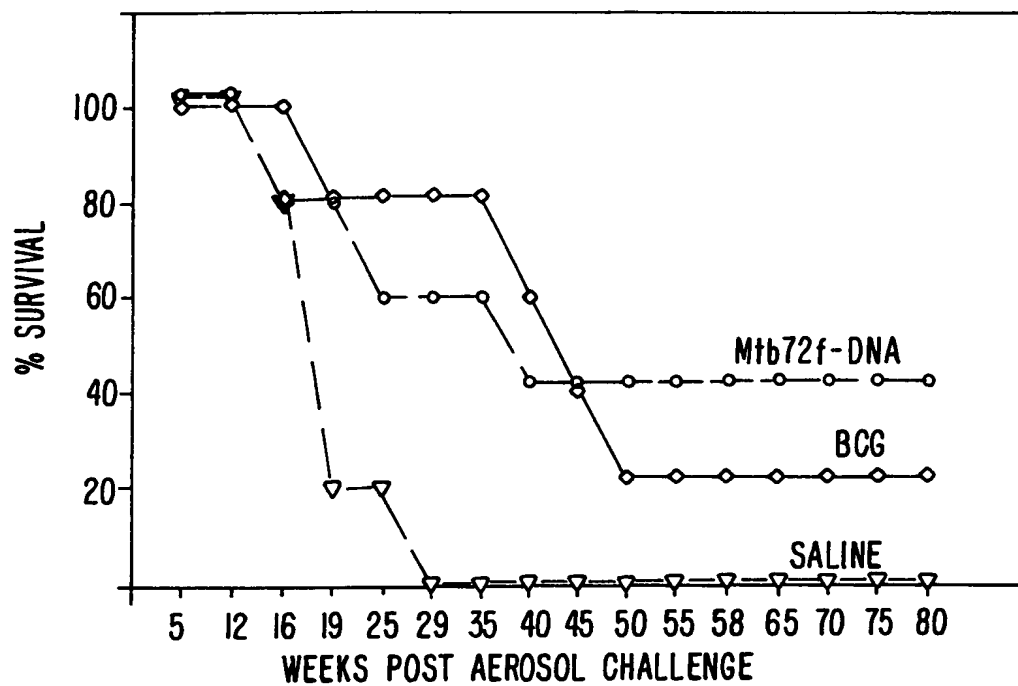
FIG. 6.

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FIG. 7.